Cross-Sectional Survey of STEC in 12 Belgian Cattle Farms

INTRODUCTION:

Cattle are regarded to as an important reservoir for shigatoxin-producing *E. coli*. Attention is especially given to the well-known O157, however the non-O157 have been increasingly isolated from human clinical cases such as (bloody) diarrhoea and HUS. A cross-sectional survey was conducted to determine the within-herd prevalence on 12 farms, tested positive for STEC O157 and/or non-O157 (O26 and/or O103) in a survey performed previously at the slaughterhouse level.

METHODS:

On each selected herd, the sample size was calculated based on 95% confidence level and 10% maximum absolute error. Rectal samples (n=463) were examined for the presence of STEC O157 and/or non-O157. Isolation of STEC O157 was performed by a 6-hour enrichment followed by IMS and selective plating on CT-SMAC. Isolation of STEC non-O157 was achieved by a 6- & 24-hour enrichment followed by direct plating and IMS prior plating on differential agar medium. Suspected colonies were transferred to one or more serotype-specific confirmation media. All suspected colonies, O157 as well as non-O157, were confirmed by PCR and examined for the presence of virulence genes by a multiplex virulence PCR.

RESULTS AND DISCUSSION:

On 75% of the herds, STEC was found in one or more faecal samples. STEC was isolated in 36 out of 463 faecal samples (7.8%) and the mean within-herd prevalence was 9.1%. As STEC has been reported to be excreted intermittently and as all samples were taken on the same moment, the within-herd prevalence may therefore be underestimated. All isolates carried *eae* and *hlyA.* Of these isolates, 15 isolates (41.5%) possessed the *stx2* gene only, whereas 34 (94.5%) had the *stx1* gene. Two herds presented more than one virulence pattern and three herds tested negative.